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EXAMINER	
SEHARASEYON, JEGATHEESAN	

ART UNIT	PAPER NUMBER
1647	

DATE MAILED: 09/17/2004

Please find below and/or attached an Office communication concerning this application or proceeding.

Office Action Summary	Application No.	Applicant(s)	
	10/063,731	EATON ET AL.	
	Examiner	Art Unit	
	Jegatheesan Seharaseyon	1647	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If the period for reply specified above is less than thirty (30) days, a reply within the statutory minimum of thirty (30) days will be considered timely.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

1)☒ Responsive to communication(s) filed on *10 September 2002*.

2a)☐ This action is **FINAL**. 2b)☒ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4)☒ Claim(s) *1-20* is/are pending in the application.

4a) Of the above claim(s) _____ is/are withdrawn from consideration.

5)☐ Claim(s) _____ is/are allowed.

6)☒ Claim(s) *1-20* is/are rejected.

7)☐ Claim(s) _____ is/are objected to.

8)☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

9)☐ The specification is objected to by the Examiner.

10)☐ The drawing(s) filed on _____ is/are: a)☐ accepted or b)☐ objected to by the Examiner.

Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).

11)☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

12)☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

a)☐ All b)☐ Some * c)☐ None of:

1.☐ Certified copies of the priority documents have been received.

2.☐ Certified copies of the priority documents have been received in Application No. _____.

3.☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

1) ☒ Notice of References Cited (PTO-892)
2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
3) ☒ Information Disclosure Statement(s) (PTO-1449 or PTO/SB/08) Paper No(s)/Mail Date *9/17/02*.
4) ☐ Interview Summary (PTO-413) Paper No(s)/Mail Date. _____ .
5) ☐ Notice of Informal Patent Application (PTO-152)
6) ☒ Other: *See Continuation Sheet*.

Continuation of Attachment(s) 6). Other: Notice to comply & Appendix A1-4.

DETAILED ACTION

1. Applicant's preliminary amendment filed on 10 September 2002 is acknowledged and entered. Claims 1-20 are pending and under consideration. The claims are drawn to the nucleotide encoding protein designated PRO1572, also identified as encoded by DNA73734-1680 and ATCC accession number 203363, shown in Figures 117 (nucleic acid) and 118 (protein).

Specification

2. The title of the invention is not descriptive. A new title is required that is clearly indicative of the invention to which the claims are directed.

3. This application contains sequence disclosures that are encompassed by the definitions for nucleotide and/or amino acid sequences set forth in 37 CFR 1.821(a)(1) and (a)(2). However, this application fails to comply with the requirements of 37 CFR 1.821 through 1.825 for the reason(s) set forth on the attached Notice To Comply With Requirements For Patent Applications Containing Nucleotide Sequence And/Or Amino Acid Sequence Disclosures. Applicant must comply with the requirements of the sequence rules (37 CFR 1.821 - 1.825). Applicant is required to provide a paper copy of the CRF in response to the Office Action.

Information Disclosure Statement

4. The information disclosure statement, filed 10/17/2002, has been considered. The BLAST results demonstrate that applicants are aware of nucleic acids with identity/homology to the one claimed herein. However, as the BLAST results do not

give sufficient identifying information, the Examiner cannot determine if said sequences constitute prior art.

Priority Determination

5. The claimed nucleotide has no utility, see rejection below. Accordingly, priority under 35 U.S.C. 120 is set at the instant filing date, 5/8/02.

Should the applicant disagree with the examiner's factual determination above, it is incumbent upon the applicant to provide the serial number and specific page number(s) of any parent application filed prior to the date recited above which specifically supports the particular claim limitation for each and every claim limitation in all the pending claims which applicant considers to have been in possession of, and fully enabled for, prior to that date.

Claim Rejections - 35 USC § 112

6. The following is a quotation of the second paragraph of 35 U.S.C. 112:

> The specification shall conclude with one or more claims particularly pointing out and distinctly claiming the subject matter which the applicant regards as his invention.

Claims 1-6, 8-10 and 14-20 are rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention.

6a. The protein identified as PRO1572 (SEQ ID NO: 118) is not disclosed as being expressed on a cell surface. Accordingly, the limitation that the claimed protein comprises an "extracellular domain" (for example see claims 1, 6 and 14 parts (c) and (d)) is indefinite, as the art does not recognize soluble proteins as having such domains. Further, if the protein had an extracellular domain, the recitation of "the extracellular

domain", "lacking its associated signal sequence" (claim 1, 6 and 14, part (d), for example) is indefinite as a signal sequence is not generally considered to be part of an extracellular domain, as signal sequences are cleaved from said domains in the process of secretion from the cell. Claims 2-5, 8-10 and 15-20 are rejected insofar as they are depended on rejected claims 1, 6 and 14.

6b. Claims that recite that the claimed polynucleotide "hybridizes to" another sequence, such as claim 14, are indefinite as there is no limiting definition of such in the specification, and the metes and bounds of that which will hybridize are dependent upon the conditions under which the hybridization is performed. As the metes and bounds of what will hybridize to a given sequence are entirely dependent upon the conditions of hybridization and washing, the metes and bounds of the claims cannot be determined. With respect to claim 15, although the further limitation that the hybridization conditions are "stringent" is introduced, the term "stringent conditions" is also a relative term, and the metes and bounds of the claim cannot be determined. Claim 15 is rejected insofar as it is depended on rejected claim 14.

Rejections under 35 U.S.C. §101 and §112

7. 35 U.S.C. 101 reads as follows:

> Whoever invents or discovers any new and useful process, machine, manufacture, or composition of matter, or any new and useful improvement thereof, may obtain a patent therefor, subject to the conditions and requirements of this title.

Claims 1-20 are rejected under 35 U.S.C. 101 because the claimed invention is not supported by either a specific, substantial and credible asserted utility or a well-established utility.

Claims 1-20 are directed to isolated polynucleotides that are 80-100% identical to (a) a sequence encoding polypeptide of SEQ ID NO: 118 or (b) a sequence encoding the polypeptide of SEQ ID NO: 118 lacking signal sequence or (c) a sequence encoding the extracellular domain of SEQ ID NO: 118 or (d) a sequence encoding the extracellular domain of the polypeptide of SEQ ID NO: 118, lacking the signal sequence or (e) a polynucleotide sequence of SEQ ID NO: 117 or (f) a full-length coding sequence of SEQ ID NO: 117 or (g) the full-length coding sequence of the cDNA deposited under ATCC 203363. Dependent claims are directed to polynucleotides that hybridize to the above sequences, vectors and host cells comprising the isolated polynucleotides. The specification discloses the isolation of a polynucleotide sequence, SEQ ID NO: 117, which encodes a protein, SEQ ID NO: 118 which is disclosed as PRO1572 (see page 21). The specification contains numerous asserted utilities the claimed nucleotides, including use as a hybridization probe, in the generation of anti-sense RNA and DNA, "knock-out" animals, as a diagnostic tool, for therapeutic purposes and for the antibody production. Further, there is no disclosure that the protein encoded by the instant nucleotides is expected to be a transmembrane protein, nor of any extracellular domain. There is no biological activity, expression pattern, phenotype, disease or condition, ligand, binding partner, or any other specific feature that is disclosed as being associated with PRO1572 provided in the specification. In the instant invention, claims are directed to polynucleotide sequences encoding the polypeptide of SEQ ID NO: 118 (PRO1572).

The polynucleotide (cDNA) encoding PRO1572 is disclosed to highly express in normal lung and compared to lung tumor based on the microarray analysis in Example 18 (see page 143, Table 7). Table 7 also describes that many other DNA's are over expressed in various tumors, based on which the specification made a general assertion that an over expressed protein in a diseased tissue is useful not only as a diagnosis marker for the presence of the disease condition, but also as a therapeutic target for treatment of the disease condition. The asserted utility in diagnosis and treatment is not substantial for the following reasons. The specification does not disclose the biological significance of this high expression levels, nor the correlation between the high/low expression of the DNA encoding protein PRO1572 and a predisposition to the onset of lung tumor, i.e., whether it is the cause or the result of the tumors. Further, there is no supporting evidence to indicate that the polypeptide encoded by the polynucleotide of the instant invention is expressed less in tumor tissues compared to their normal tissue counterparts, and as such one of skilled in the art would conclude that it is not supported by a substantial asserted utility or a well-established utility.

Although, the specification claims that the polynucleotide is more highly expressed in the normal lung, the specification does not teach what is the normal level of expression, does not indicate how high the expression level is compared to for example, lung tumor; and does not provide a statistical correlation to the level of expression (for example, there is no indication of how many samples were compared to study the expression). Furthermore, even if the tumor is malignant, the specification fails

to describe the type or kind of tumor present in lung (for example, is it an adenocarcinoma or sarcoma etc.). Without knowing the identity of the tumors, one of skill in art cannot use the polynucleotides for diagnosis or therapeutic purposes as asserted. The specification does not disclose a correlation between any specific disorder and the altered level or form of the claimed polypeptides. In addition, the specification does not teach or describe the function of this yet to be identified polypeptide. With respect to the remaining utilities, none of these asserted utilities is specific for the disclosed PRO1572 encoding polypeptides, as each of the aforementioned utilities could be asserted for any naturally occurring polypeptides, and further, as none of the asserted utilities requires any feature or activity that is specific to the disclosed PRO1572 polypeptides.

The polynucleotide may have utility because either its presence or absence or elevation or reduction is correlated to a disease. If this is not the case, then one must turn to the protein encoded by said polynucleotide to ask, "Does the protein encoded by the polynucleotide have utility?" This is a critical question because if the protein has utility, then this confers utility upon the polynucleotide from which it is transcribed or translated. However, there is no supporting evidence to indicate that the polypeptide encoded by the nucleotide of the instant invention is more highly expressed in tumor containing lung, colon and breast tissues compared to the normal lung, colon and breast tissues. Therefore, one skilled in the art would conclude that it is not supported by a substantial asserted utility or a well-established utility.

Cancerous tissue is known to be aneuploid, that is, having an abnormal number of chromosomes (see Sen, 2000, Curr. Opin. Oncol. 12: 82-88). The data presented in the instant specification are not corrected for aneuploidy. A higher amplification of a gene does not necessarily mean higher expression or lower in a tissue, but can merely be an indication that the cancer tissue is aneuploid. The preliminary data of the instant invention was not supported by further analysis of mRNA or protein expression, for example. Also, the literature reports that it does not necessarily follow that an increase in gene copy number results in increased gene expression and increased polypeptide expression, such that the claimed polypeptides would be useful for diagnosis of cancer or as a drug target. In addition, there is no correlation between WISP-2 mRNA expression and colon tumors. This fact is documented by Pennica et al. (1998, PNAS USA 95:14717-14722). In addition, they also observed that there was no correlation between WISP-2 mRNA expression and colon tumors. Furthermore they disclose that:

> "An analysis of *WISP*-1 gene amplification and expression in human colon tumors showed a correlation between DNA amplification and overexpression, whereas overexpression of *WISP*-3 RNA was seen in the absence of DNA amplification. In contrast, *WISP*-2 DNA was amplified in the colon tumors, but its mRNA expression was significantly reduced in the majority of tumors compared with the expression in normal colonic mucosa from the same patient."

See p. 14722, second paragraph of left column; pp. 14720-14721, "Amplification and Aberrant Expression of *WISPs* in Human Colon Tumors." For example, WISP-2 RNA expression was significantly lower in the tumor than the mucosa (see p. 14721). Therefore, one cannot extrapolate the expression data provided in the specification to support the implicit assertion that the polynucleotide encoding PRO1572 can be used in cancer diagnosis or therapy.

The instant application has failed to provide guidance as to how one of skill in the art could use the claimed invention in a way that constitutes a substantial utility. The proposed uses of the claimed invention are simply starting points for further research and investigation into potential practical uses of the claimed nucleotides encoding the polypeptides. "Congress intended that no patent be granted on a chemical compound whose sole 'utility' consists of its potential role as an object of use-testing." Brenner v. Manson, 148 USPQ: at 696.

A substantial utility, by definition, is a utility the defines "real world" use, and a utility that requires or constitutes carrying out further research to identify or reasonably confirm a "real world" context of use is not substantial utility. In the instant case, the higher expression of the nucleotides encoding PRO1572 in normal lung compared to tissue with lung tumor (if significant), at the most, is an interesting invitation for further research, experimentation and confirmation as to whether the PRO1572 is useful as a diagnosis marker, or suitable as a therapeutic target for treatment of the tumors. These further research and experimentation, however, is part of the act of invention, and until it has been undertaken, the claimed invention is not considered substantial.

8. The following is a quotation of the first paragraph of 35 U.S.C. 112:

> The specification shall contain a written description of the invention, and of the manner and process of making and using it, in such full, clear, concise, and exact terms as to enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the same and shall set forth the best mode contemplated by the inventor of carrying out his invention.

8a. Claims 1-20 are also rejected under 35 U.S.C. 112, first paragraph. Specifically, since the claimed invention is not supported by either a specific and substantial asserted utility or a well established utility for the reasons set forth above (Paragraph 6), one skilled in the art clearly would not know how to use the polynucleotide of SEQ ID NO: 117 nor polynucleotides 80, 85, 90, 95 or 99% identical to such, nor which encode a protein 80, 85, 90, 95 or 99% identical to the protein of SEQ ID NO: 118, nor polynucleotides which hybridize to any of the above.

Furthermore, even if a specific and substantial utility were subsequently established they would be enabled only for the polynucleotide of SEQ ID NO: 117 or fragments of such that are usable as hybridization probes and are not enabled for polynucleotides 80, 85, 90, 95 or 99% identical to such, nor which encode a protein 80, 85, 90, 95 or 99% identical to the protein of SEQ ID NO: 118, nor polynucleotides which hybridize to any of the above because there is n no structural or functional information provided in the specification.

The factors considered when determining if the disclosure satisfies the enablement requirement and whether any necessary experimentation is "undue" include, but are not limited to:

1) nature of the invention, 2) state of the prior art, 3) relative skill of those in the art, 4) level of predictability in the art, 5) existence of working examples, 6) breadth of claims, 7) amount of direction or guidance by the inventor, and 8) quantity of experimentation

needed to make or use the invention. In re *Wands*, 858 F.2d 731, 737, 8 USPQ2d 1400, 1404 (Fed. Cir. 1988).

The claims are directed to isolated polynucleotides having at least 80% identity to a SEQ ID NO: 117 or that encode the protein of SEQ ID NO: 118 with or without its signal peptide, or which encode the extracellular domain of SEQ ID NO: 118 with or without its signal peptide, or polynucleotides at least 80% identical to such encoding polynucleotides. Dependent claims are directed to polynucleotides that hybridize to the above sequences, vectors and host cells comprising the isolated polynucleotides. In the instant application, there is insufficient guidance regarding how to make PRO1572 polynucleotides variants recited in the claims.

The specification also is not enabling for the breadth of claims to polynucleotide molecules that hybridize to the disclosed sequences. It is noted that claims that recite hybridization language fail to provide adequate guidance, and do not recite that the polynucleotide encodes a protein, much less one having a specifically disclosed activity. First of all, it is pointed out that the term "hybridize" or "hybridization" generically refers to a process in which a strand of polynucleotide joins or matches up with a complementary strand through the process of base pairing, wherein the process is basically used to locate or identify DNAs encoding specific proteins. It is well established in the art that 15-20 bases have been considered sufficient to achieve this process. The breadth of the claims includes polynucleotides of as little as 10 nucleotides. With these points in mind, it is the Examiner's position that giving the claims their broadest reasonable interpretation, this language reads on an infinite number of possible DNA sequences for which there is not sufficient enablement without

undue experimentation because of the breath of claims, the lack of guidance provided and the quantity of experimentation needed to make or use the invention.

With respect to the hybridization use, as discussed above in paragraph 6 the invention lacks utility and thus lacks enablement. Even if utility were established, the enablement is commensurate in scope only with claims to polynucleotides that are fragments of SEQ ID NO: 117, said fragments of sufficient length to be used as hybridization probes or primers. However, enablement is *not* commensurate in scope with fragments of polynucleotides that differ from SEQ ID NO: 117 due to codon degeneracy, as it is not recognized in the art to use such sequences that are degenerate for such detection or synthesis, and the specification provides no guidance as to how or why to make such degenerate probes or primers. The specification also is not enabling for the breadth of claims to polynucleotide molecules that hybridize to the disclosed sequences because of the quantity of experimentation needed and the lack of guidance provided by the inventor.

The examples provided in the specification do not provide working examples of different DNA sequences that would enable a representative number of the above discussed DNA sequences with assurances that they can be used as probes or primers for the purpose of amplifying or detecting the PRO1572 gene. The mere recitation of this term, and the definitions provided do not serve as sufficient guidance to enable the breadth of the claims for the various DNA sequences claimed. See Ex parte *Forman*, 230 USPQ 546. Since the first paragraph of the statute under 35 U.S.C. 112 requires that there must be an enabling disclosure to support the breadth of the Claims, a review

of the specification confirms that the scope of the various DNA sequences that are discussed above have not been enabled. There is but a single polynucleotide disclosed with reference to PRO1572, SEQ ID NO: 117. In the absence of working examples, breadth of claims and sufficient guidance, it would require undue experimentation to enable a commensurate number of the sequences that are encompassed by the claims.

Since the claimed polynucleotides are described at least in part in terms of the protein that might be encoded, the scope of the protein itself must be considered: The specification asserts that PRO1572 is an unspecified secreted and transmembrane polypeptide. However, this family of proteins does not possess a common utility, but rather the proteins that can be broadly classified and have different activities, that confer different uses on them. Accordingly, the mere identification of a protein as belonging to a family, while indicative of evolutionary relatedness, is not indicative of function, nor by extension, of utility. The structure of the putative PRO1572 peptide is briefly discussed in Figure 118, as having a putative signal sequence, corresponding to amino acids 1-23. It also describes transmembrane domain, corresponding to about amino acids 81-100, 121-141 and 173-194.

The problem of predicting protein structure from sequence data and in turn utilizing predicted structural determinations to ascertain functional aspects of the protein is extremely complex. While it is known that many amino acid substitutions are generally possible in any given protein, the positions within the protein's sequence where such amino acid substitutions can be made with a reasonable expectation of success are limited. Certain positions in the sequence are critical to the protein's

structure/function relationship, e.g. such as various sites or regions directly involved in binding, activity and in providing the correct three-dimensional spatial orientation of binding and active sites. However, Applicant has provided little or no guidance beyond the mere presentation of sequence data to enable one of ordinary skill in the art to determine, without undue experimentation, the positions in the protein which are tolerant to change (e.g. such as by amino acid substitutions or deletions), and the nature and extent of changes that can be made in these positions. Therefore, undue experimentation would be required of the skilled artisan to make and/or use the claimed invention in its full scope, i.e. all the polynucleotides with the various percent identities.

8b. Claims 1-5 and 15-20 are rejected under 35 U.S.C. 112, first paragraph, as containing subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention.

To provide evidence of possession of a claimed genus, the specification must provide sufficient distinguishing identifying characteristics of the genus. The factors to be considered include disclosure of compete or partial structure, physical and/or chemical properties, functional characteristics, structure/function correlation, methods of making the claimed product, or any combination thereof.

The claims are drawn to polynucleotides having at least 80%, 85%, 95% or 99% sequence identity with a particular disclosed sequence, or that merely hybridize to a disclosed sequence. The claims do not require that the claimed polynucleotide encode

a particular protein, nor that any protein encoded thereby possess any particular biological activity, nor any particular conserved structure, or other disclosed distinguishing feature. The specification teaches that PRO1572 has (unspecified) homology to secreted and transmembrane polypeptide. The structure of the putative PRO1572 peptide is briefly discussed in Figure 118, as having a putative signal sequence, corresponding to amino acids 1-23. It also describes transmembrane domain, corresponding to about amino acids 81-100, 121-141 and 173-194. However, there is no functional characteristic associated with these motifs, hence the mere observation that they exist is not probative of function or utility. Further, there is no disclosure that the protein is expected to be a transmembrane protein, nor of any extracellular domain. In this case, the only factor present in the claim is a partial structure in the form of a recitation of percent identity. There is not even identification of any particular portion of the structure that must be conserved. Accordingly, in the absence of sufficient recitation of distinguishing identifying characteristics, the specification does not provide adequate written description of the claimed genus.

Vas-Cath Inc. v. Mahurkar, 19 USPQ2d 1111, clearly states that "applicant must convey with reasonable clarity to those skilled in the art that, as of the filing date sought, he or she was in possession *of the invention*. The invention is, for purposes of the 'written description' inquiry, *whatever is now claimed.*" (See page 1117.) The specification does not "clearly allow persons of ordinary skill in the art to recognize that [he or she] invented what is claimed." (See *Vas-Cath* at page 1116). As discussed above, the skilled artisan cannot envision the detailed chemical structure of the

encompassed genus of polypeptides, and therefore conception is not achieved until reduction to practice has occurred, regardless of the complexity or simplicity of the method of isolation. Adequate written description requires more than a mere statement that it is part of the invention and reference to a potential method of isolating it. The compound itself is required. See *Fiers v. Revel*, 25 USPQ2d 1601 at 1606 (CAFC 1993) and *Amgen Inc. v. Chugai Pharmaceutical Co. Ltd.*, 18 USPQ2d 1616.

One cannot describe what one has not conceived. See *Fiddes v. Baird*, 30 USPQ2d 1481 at 1483. In *Fiddes*, claims directed to mammalian FGF's were found to be unpatentable due to lack of written description for that broad class. The specification provided only the human sequence.

Therefore, polynucleotides comprising the sequence set forth in SEQ ID NO: 117 or encoding the protein of SEQ ID NO: 118, or fragments thereof sufficiently long to be used as hybridization probes but not the full breadth of the claims meet the written description provision of 35 U.S.C. 112, first paragraph. Applicant is reminded that *Vas-Cath* makes clear that the written description provision of 35 U.S.C. 112 is severable from its enablement provision (see page 1115).

Claim Rejections - 35 USC § 102

9. The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that form the basis for the rejections under this section made in this Office action:

> A person shall be entitled to a patent unless :
>
> (b) the invention was patented or described in a printed publication in this or a foreign country or in public use or on sale in this country, more than one year prior to the date of application for patent in the United States.

9a. Claims 1-10 and 12-20 are rejected under 35 U.S.C. 102(b) as being anticipated by Sheppard et al. (WO 00/15659 A2, 22 March 2000).

Sheppard et al. et al discloses an amino acid sequence that has 100% overall identity to SEQ ID NO: 118 of the instant invention (Appendix A1-A2). The reference also describes the full length coding (cDNA) sequence (Appendix A3-A4). Thus, meeting the limitations of claims 1-7, 9, 12 and 13. In addition, given this sequence identity the sequence of Sheppard et al. would hybridize under stringent conditions (claims 14-16). The amino acid described by the instant invention (SEQ ID NO: 118) is encoded SEQ ID NO: 1 describe by Sheppard et al. Further, Sheppard et al. have described the expression of nucleotides containing vectors with promoter sequences in hosts cells (pages: 38-40). With respect to the limitation of "lacking its associated signal peptide" in claims 8 and 10 as Sheppard et al. teaches recombinant expression of the said polypeptide, the cDNA would produce the polypeptide identical to the present SEQ ID NO: 118, but lacking its associated signal peptide when transfected into the host cell. Thus, meeting the limitations of claims 8, 10 and 17-20. Therefore, claims 1-10 and 12-20 are rejected as being anticipated by Sheppard et al. (WO 00/15659 A2, 22 March 2000).

10. No claims are allowed.

Contact Information

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Jegatheesan Seharaseyon whose telephone number is 571-272-0892. The examiner can normally be reached on M-F: 8:30-4:30.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Brenda Brumback can be reached on 571-272-0961. The fax phone number for the organization where this application or proceeding is assigned is 703-872-9306.

Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see http://pair-direct.uspto.gov. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free).

JS 09/04

Brenda Brumback
BRENDA BRUMBACK
SUPERVISORY PATENT EXAMINER
TECHNOLOGY CENTER 1600

XX
PS Claim 11; Page 772; 5507pp; English.
XX
CC AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397,
CC which represent the human ORFX open reading frames 1 to 3161. The ORFX
CC sequences have activities such as: cytostatic; hepatotropic; vulnerary;
CC antipsoriatic; antiparkinsonian; nootropic; neuroprotective; osteopathic;
CC anticonvulsant; antiarthritic; immunosuppressant; immunostimulant;
CC cardiant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive;
CC dermatological; immunosuppressive; antiinflammatory; antibacterial;
CC antiviral; antifungal; antirheumatic; antithyroid; and antianaemic. The
CC sequences can be used for determining the presence of or predisposition
CC to, or preventing or treating pathological conditions associated with an
CC ORFX-associated disorder. The nucleic acids can be used to express ORFX
CC proteins in gene therapy vectors. The proteins and nucleic acids may be
CC used to treat cancers, proliferative disorders, neurodegenerative
CC disorders, osteoarthritis, graft vs host disease, cardiovascular disease,
CC diabetes mellitus, hypertension, hypothyroidism, cholesterol ester
CC storage, systemic lupus erythematosus, severe combined immunodeficiency
CC (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune
CC disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and
CC cartilage damage, nocturnal haemoglobinuria, antiinflammatory disease; to
CC enhance coagulation; to inhibit thrombosis; and as a contraceptive
XX
SQ Sequence 261 AA;

Query Match 100.0%; Score 1357; DB 3; Length 261;
Best Local Similarity 100.0%; Pred. No. 8e-144;
Matches 261; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MSTTTCQVVAFLLSILGLAGCIAATGMDMWSTQDLYDNPVTSVFQYEGLWRSCVRQSSGF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MSTTTCQVVAFLLSILGLAGCIAATGMDMWSTQDLYDNPVTSVFQYEGLWRSCVRQSSGF 60

Qy         61 TECRPYFTILGLPAMLQAVRALMIVGIVLGAIGLLVSIFALKCIRIGSMEDSAKANMTLT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TECRPYFTILGLPAMLQAVRALMIVGIVLGAIGLLVSIFALKCIRIGSMEDSAKANMTLT 120

Qy        121 SGIMFIVSGLCAIAGVSVFANMLVTNFWMSTANMYTGMGGMVQTVQTRYTFGAALFVGWV 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SGIMFIVSGLCAIAGVSVFANMLVTNFWMSTANMYTGMGGMVQTVQTRYTFGAALFVGWV 180

Qy        181 AGGLTLIGGVMMCIACRGLAPEETNYKAVSYHASGHSVAYKPGGFKASTGFGSNTKNKKI 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AGGLTLIGGVMMCIACRGLAPEETNYKAVSYHASGHSVAYKPGGFKASTGFGSNTKNKKI 240

Qy        241 YDGGARTEDEVQSYPSKHDYV 261
              |||||||||||||||||||||
Db        241 YDGGARTEDEVQSYPSKHDYV 261
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RESULT 2
AAY70675
ID AAY70675 standard; protein; 261 AA.
XX
AC AAY70675;
XX
DT 18-JUL-2000 (first entry)
XX
DE Human stomach protein zsig28.
XX
KW Human; stomach; zsig28 protein; chromosome 3q22.1-3q22.2; gene therapy;
KW claudin; oligodendrocyte-specific protein; OSP; apoptosis; RVP.1;
KW rat androgen-withdrawal apoptosis protein; growth factor receptor;
KW cell-cell signalling molecule; cytostatic; antibacterial; food poisoning;
KW Botulism; diarrhoea; inflammation; cramping; cancer; gastric ulcer;
KW diagnosis; prevention; treatment.
XX
OS Homo sapiens.
XX

FH	Key	Location/Qualifiers
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FT	Protein	24. .261
FT		/label= Mature_zsig28_protein
FT	Region	24. .82
FT		/label= Region_1
FT		/note= "useful as antigenic epitope for antibody production"
FT	Region	48. .54
FT		/label= Motif_1
FT		/note= "Conserved and low variance motif"
FT	Region	77. .82
FT		/label= Motif_2
FT		/note= "Conserved and low variance motif"
FT	Domain	83. .100
FT		/label= Transmembrane_domain
FT	Region	101. .122
FT		/label= Region_2
FT		/note= "useful as antigenic epitope for antibody production"
FT	Domain	123. .140
FT		/label= Transmembrane_domain
FT	Region	141. .174
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FT		/note= "useful as antigenic epitope for antibody production"
FT	Region	174. .180
FT		/label= Motif_3
FT		/note= "Conserved and low variance motif"
FT	Domain	175. .192
FT		/label= Transmembrane_domain
FT	Region	184. .189
FT		/label= Motif_4
FT		/note= "Conserved and low variance motif"
FT	Region	193. .261
FT		/label= Region_4
FT		/note= "hydrophilic region useful as antigenic epitope for antibody production"

XX
PN WO200015659-A2.
XX
PD 23-MAR-2000.
XX
PF 14-SEP-1999; 99WO-US021023.
XX
PR 16-SEP-1998; 98US-00154444.
XX
PA (ZYMO) ZYMOGENETICS INC.
XX
PI Sheppard PO, Foley KP;
XX
DR WPI; 2000-271379/23.
DR N-PSDB; AAZ52249.
XX
PT New isolated polynucleotide encoding a stomach zsig28 polypeptide used
PT for diagnosis, prevention and treatment of stomach disorders caused by
PT bacteria, gastric ulcers or cancer.
XX
PS Claim 12; Page 113-114; 121pp; English.
XX
CC The present sequence is a stomach protein zsig28 from human lung library.
CC The zsig28 gene is located at 3q22.1-3q22.2 region of human chromosome 3.
CC The protein shows homology to a diverse family of receptor proteins
CC containing e.g. human claudin 1 and 2, human and murine oligodendrocyte-
CC specific protein (OSP) and rat androgen-withdrawal apoptosis protein
CC RVP.1. It is thought to be a cell-cell signalling molecule, a growth
CC factor receptor or extracellular matrix associated protein with growth
CC factor hormone activity and may be involved in an apoptotic cellular
CC pathway. The protein may act as an anti-microbial agent and may bind
CC toxins produced by bacteria which cause food poisoning, Botulism, severe
CC diarrhoea, inflammation and cramping. zsig28 agonists are useful for
CC promoting apoptosis in cells over-expressing zsig28 e.g. in cancer cells.
CC They are also useful for stimulating cell growth or differentiation.
CC Altered levels of zsig28 protein in a test sample such as saliva, serum,
CC sweat or biopsy can be monitored as an indication of digestive function,

Fri

CC gastric ulcer or cancer. zsig28 expression can be used as a
CC differentiation marker to determine the stage of tumour or cell maturity,
CC particularly in epithelial cells. Polynucleotides encoding zsig28 can be
CC used in gene therapy applications to increase or inhibit zsig28 activity
XX
SQ Sequence 261 AA;

Query Match 100.0%; Score 1357; DB 3; Length 261;
Best Local Similarity 100.0%; Pred. No. 8e-144;
Matches 261; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db          1 MSTTTCQVVAFLLSILGLAGCIAATGMDMWSTQDLYDNPVTSVFQYEGLWRSCVRQSSGF 60

Qy         61 TECRPYFTILGLPAMLQAVRALMIVGIVLGAIGLLVSIFALKCIRIGSMEDSAKANMTLT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TECRPYFTILGLPAMLQAVRALMIVGIVLGAIGLLVSIFALKCIRIGSMEDSAKANMTLT 120

Qy        121 SGIMFIVSGLCAIAGVSVFANMLVTNFWMSTANMYTGMGGMVQTVQTRYTFGAALFVGWV 180
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Db        121 SGIMFIVSGLCAIAGVSVFANMLVTNFWMSTANMYTGMGGMVQTVQTRYTFGAALFVGWV 180

Qy        181 AGGLTLIGGVMMCIACRGLAPEETNYKAVSYHASGHSVAYKPGGFKASTGFGSNTKNKKI 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AGGLTLIGGVMMCIACRGLAPEETNYKAVSYHASGHSVAYKPGGFKASTGFGSNTKNKKI 240

Qy        241 YDGGARTEDEVQSYPSKHDYV 261
              |||||||||||||||||||||
Db        241 YDGGARTEDEVQSYPSKHDYV 261
```

RESULT 3
AAY92235
ID AAY92235 standard; protein; 261 AA.
XX
AC AAY92235;
XX
DT 10-AUG-2000 (first entry)
XX
DE Claudin homologue from clone 3224646 cDNA.
XX
KW Clone 3224646; claudin; homologue; cytostatic; anti-HIV;
KW immunosuppressive; antiallergic; antiinfective; antiinflammatory;
KW antiarthritic; antiarteriosclerotic; vasotropic; neuroprotective;
KW nootropic; dermatological; tranquilizer; vulnerary.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1. .23
FT /label= signal_peptide
FT Protein 23. .261
FT /label= mature_protein
XX
PN WO200020447-A2.
XX
PD 13-APR-2000.
XX
PF 06-OCT-1999; 99WO-US023294.
XX
PR 06-OCT-1998; 98US-0103195P.
PR 05-OCT-1999; 99US-00412231.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Shimkets RA;
XX
DR WPI; 2000-303741/26.
DR N-PSDB; AAA09116, AAA09121.
XX
PT Nucleic acids encoding polypeptides with syncline-like, claudin-like or
PT cytokine-like activity, useful for treating diseases including cancer,
PT Alzheimer's and atherosclerosis.
XX
PS Claim 20; Fig 3A; 118pp; English.
XX
CC Clone 3223867 encodes a polypeptide that has homology to claudin-1, which
CC is an integral membrane protein found in tight junctions. The sequences
CC are useful for treatment of diseases such as cancer, immune disorders,
CC autoimmune disease, acquired immune deficiency syndrome (AIDS),
CC transplant rejection, allergy, infection by a pathological agent or
CC organism, inflammatory disorders, arthritis, a haematopoietic disorder, a
CC skin disorder, atherosclerosis, restenosis, a neurological disease,
CC Alzheimer's disease, trauma, spinal cord injury and skeletal disorders
XX
SQ Sequence 261 AA;

Query Match 100.0%; Score 1357; DB 3; Length 261;
Best Local Similarity 100.0%; Pred. No. 8e-144;
Matches 261; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MSTTTCQVVAFLLSILGLAGCIAATGMDMWSTQDLYDNPVTSVFQYEGLWRSCVRQSSGF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy         61 TECRPYFTILGLPAMLQAVRALMIVGIVLGAIGLLVSIFALKCIRIGSMEDSAKANMTLT 120
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Db         61 TECRPYFTILGLPAMLQAVRALMIVGIVLGAIGLLVSIFALKCIRIGSMEDSAKANMTLT 120

Qy        121 SGIMFIVSGLCAIAGVSVFANMLVTNFWMSTANMYTGMGGMVQTVQTRYTFGAALFVGWV 180
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Db        121 SGIMFIVSGLCAIAGVSVFANMLVTNFWMSTANMYTGMGGMVQTVQTRYTFGAALFVGWV 180

Qy        181 AGGLTLIGGVMMCIACRGLAPEETNYKAVSYHASGHSVAYKPGGFKASTGFGSNTKNKKI 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AGGLTLIGGVMMCIACRGLAPEETNYKAVSYHASGHSVAYKPGGFKASTGFGSNTKNKKI 240

Qy        241 YDGGARTEDEVQSYPSKHDYV 261
              |||||||||||||||||||||
Db        241 YDGGARTEDEVQSYPSKHDYV 261
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RESULT 4
AAY99432
ID AAY99432 standard; protein; 261 AA.
XX
AC AAY99432;
XX
DT 08-AUG-2000 (first entry)
XX
DE Human PRO1572 (UNQ778) amino acid sequence SEQ ID NO:326.
XX
KW Human; PRO polypeptide; membrane bound protein; receptor; diagnosis;
KW transmembrane; secretion; immunoadhesion; pharmaceutical; screening.
XX
OS Homo sapiens.
XX
PN WO200012708-A2.
XX
PD 09-MAR-2000.
XX
PF 01-SEP-1999; 99WO-US020111.
XX
PR 01-SEP-1998; 98US-0098716P.
PR 01-SEP-1998; 98US-0098749P.
PR 01-SEP-1998; 98US-0098750P.
PR 02-SEP-1998; 98US-0098803P.
PR 02-SEP-1998; 98US-0098821P.
PR 02-SEP-1998; 98US-0098843P.
PR 09-SEP-1998; 98US-0099536P.
PR 09-SEP-1998; 98US-0099596P.
PR 09-SEP-1998; 98US-0099598P.
PR 09-SEP-1998; 98US-0099602P.
PR 09-SEP-1998; 98US-0099642P.
PR 10-SEP-1998; 98US-0099741P.

GenCore version 5.1.6

OM protein - nucleic search, using frame_plus_p2n model

Run on: September 2, 2004, 20:04:09 ; Search time 327 Seconds
(without alignments)
3390.764 Million cell updates/sec

Title: US-10-063-731-118
Perfect score: 1357
Sequence: 1 MSTTTCQVVAFLLSILGLAG.....DGGARTEDEVQSYPSKHDYV 261

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-Q=/cgn2_1/USPTO_spool/US10063731/runat_01092004_155041_18736/app_query.fasta_1.455
-DB=N_Geneseq_29Jan04 -QFMT=fastap -SUFFIX=rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10063731_@CGN_1_1_352_@runat_01092004_155041_18736 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N_Geneseq_29Jan04:*
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3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002s:*
7: geneseqn2003as:*
8: geneseqn2003bs:*
9: geneseqn2003cs:*
10: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		1357	100.0	982	3	AAZ52249	Aaz52249 Human sto
2		1357	100.0	1505	3	AAC74775	Aac74775 Human ORF
c 3		1357	100.0	1530	3	AAA09120	Aaa09120 Clone 322
4		1357	100.0	1530	3	AAA09116	Aaa09116 Clone 322
5		1357	100.0	1869	6	ABK81817	Abk81817 DNA repre
6		1357	100.0	2108	4	AAF54432	Aaf54432 DNA encod
7		1357	100.0	2121	3	AAA37114	Aaa37114 Human PRO
8		1357	100.0	2121	4	AAS46102	Aas46102 Human DNA
9		1357	100.0	2121	4	AAF92116	Aaf92116 Human PRO
10		1357	100.0	2121	6	ABS74436	Abs74436 Human cDN
11		1357	100.0	2121	7	ABX78705	Abx78705 Human PRO
12		1357	100.0	2121	7	ACA75677	Aca75677 Novel hum
13		1357	100.0	2121	7	ACA71157	Aca71157 Human sec
14		1357	100.0	2121	7	ACC87685	Acc87685 Human sec
15		1357	100.0	2121	7	ACC87071	Acc87071 Human sec
16		1357	100.0	2121	7	ACD04244	Acd04244 Human sec
17		1357	100.0	2121	7	ACA69575	Aca69575 cDNA enco
18		1357	100.0	2121	7	ACA90420	Aca90420 Novel hum
19		1357	100.0	2121	7	ACC89527	Acc89527 Human sec
20		1357	100.0	2121	7	ACA98318	Aca98318 Novel hum
21		1357	100.0	2121	7	ACA93960	Aca93960 Human sec
22		1357	100.0	2121	7	ACD15353	Acd15353 Human sec
23		1357	100.0	2121	7	ACD08940	Acd08940 Human sec
24		1357	100.0	2121	7	ACC96860	Acc96860 Human sec
25		1357	100.0	2121	7	ACF15581	Acf15581 Human sec
26		1357	100.0	2121	7	ACA72948	Aca72948 Human PRO
27		1357	100.0	2121	7	ACD03120	Acd03120 Novel hum
28		1357	100.0	2121	7	ACD01935	Acd01935 Novel hum
29		1357	100.0	2121	7	ACA92127	Aca92127 Novel hum
30		1357	100.0	2121	7	ACA89552	Aca89552 cDNA enco
31		1357	100.0	2121	7	ACA73562	Aca73562 Human sec
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33		1357	100.0	2121	7	ACA66711	Aca66711 cDNA enco
34		1357	100.0	2121	7	ACA91222	Aca91222 Novel hum
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ALIGNMENTS

RESULT 1
AAZ52249
ID AAZ52249 standard; DNA; 982 BP.
XX
AC AAZ52249;
XX
DT 18-JUL-2000 (first entry)
XX
DE Human stomach protein zsig28 DNA.
XX
KW Human; stomach; zsig28 protein; chromosome 3q22.1-3q22.2; gene therapy;
KW claudin; oligodendrocyte-specific protein; OSP; apoptosis; RVP.1;
KW rat androgen-withdrawal apoptosis protein; growth factor receptor;
KW cell-cell signalling molecule; cytostatic; antibacterial; food poisoning;
KW Botulism; diarrhoea; inflammation; cramping; cancer; gastric ulcer;
KW diagnosis; prevention; treatment; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
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FT sig_peptide 70. .138
FT /*tag= b
FT mat_peptide 139. .852
FT /*tag= c
FT /product= "Mature zsig28"
XX
PN WO200015659-A2.
XX
PD 23-MAR-2000.

[redacted]

Applicant's copy

Appendix A4.

XX
PF 14-SEP-1999; 99WO-US021023.
XX
PR 16-SEP-1998; 98US-00154444.
XX
PA (ZYMO) ZYMOGENETICS INC.
XX
PI Sheppard PO, Foley KP;
XX
DR WPI; 2000-271379/23.
DR P-PSDB; AAY70675.
XX
PT New isolated polynucleotide encoding a stomach zsig28 polypeptide used
PT for diagnosis, prevention and treatment of stomach disorders caused by
PT bacteria, gastric ulcers or cancer.
XX
PS Claim 2; Page 111-113; 121pp; English.
XX
CC The present sequence is a stomach protein zsig28 encoding DNA located at
CC 3q22.1-3q22.2 region of human chromosome 3 and isolated from human lung
CC library. The zsig28 protein shows homology to a diverse family of
CC receptor proteins containing e.g. human claudin 1 and 2, human and murine
CC oligodendrocyte-specific protein (OSP) and rat androgen-withdrawal
CC apoptosis protein RVP.1. It is thought to be a cell-cell signalling
CC molecule, a growth factor receptor or extracellular matrix associated
CC protein with growth factor hormone activity and may be involved in an
CC apoptotic cellular pathway. The protein may act as an anti-microbial
CC agent and may bind toxins produced by bacteria which cause food
CC poisoning, Botulism, severe diarrhoea, inflammation and cramping. zsig28
CC agonists are useful for promoting apoptosis in cells over-expressing
CC zsig28 e.g. in cancer cells. They are also useful for stimulating cell
CC growth or differentiation. Altered levels of zsig28 protein in a test
CC sample such as saliva, serum, sweat or biopsy can be monitored as an
CC indication of digestive function, gastric ulcer or cancer. zsig28
CC expression can be used as a differentiation marker to determine the stage
CC of tumour or cell maturity, particularly in epithelial cells.
CC Polynucleotides encoding zsig28 can be used in gene therapy applications
CC to increase or inhibit zsig28 activity
XX
SQ Sequence 982 BP; 218 A; 275 C; 271 G; 218 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	3.4e-149	Length:	982
Score:	1357.00	Matches:	261
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	3	Gaps:	0

US-10-063-731-118 (1-261) x AAZ52249 (1-982)

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Qy         21 CysIleAlaAlaThrGlyMetAspMetTrpSerThrGlnAspLeuTyrAspAsnProVal 40
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Qy         61 ThrGluCysArgProTyrPheThrIleLeuGlyLeuProAlaMetLeuGlnAlaValArg 80
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Db        250 ACCGAATGCAGGCCCTATTTCACCATCCTGGGACTTCCAGCCATGCTGCAGGCAGTGCGA 309

Qy         81 AlaLeuMetIleValGlyIleValLeuGlyAlaIleGlyLeuLeuValSerIlePheAla 100
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Db        310 GCCCTGATGATCGTAGGCATCGTCCTGGGTGCCATTGGCCTCCTGGTATCCATCTTTGCC 369

Qy        101 LeuLysCysIleArgIleGlySerMetGluAspSerAlaLysAlaAsnMetThrLeuThr 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        370 CTGAAATGCATCCGCATTGGCAGCATGGAGGACTCTGCCAAAGCCAACATGACACTGACC 429

Qy        121 SerGlyIleMetPheIleValSerGlyLeuCysAlaIleAlaGlyValSerValPheAla 140
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Qy        141 AsnMetLeuValThrAsnPheTrpMetSerThrAlaAsnMetTyrThrGlyMetGlyGly 160
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Qy        161 MetValGlnThrValGlnThrArgTyrThrPheGlyAlaAlaLeuPheValGlyTrpVal 180
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Qy        181 AlaGlyGlyLeuThrLeuIleGlyGlyValMetMetCysIleAlaCysArgGlyLeuAla 200
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Qy        201 ProGluGluThrAsnTyrLysAlaValSerTyrHisAlaSerGlyHisSerValAlaTyr 220
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Db        670 CCAGAAGAAACCAACTACAAAGCCGTTTCTTATCATGCCTCAGGCCACAGTGTTGCCTAC 729

Qy        221 LysProGlyGlyPheLysAlaSerThrGlyPheGlySerAsnThrLysAsnLysLysIle 240
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Db        730 AAGCCTGGAGGCTTCAAGGCCAGCACTGGCTTTGGGTCCAACACCAAAAACAAGAAGATA 789

Qy        241 TyrAspGlyGlyAlaArgThrGluAspGluValGlnSerTyrProSerLysHisAspTyr 260
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Qy        261 Val 261
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Db        850 GTG 852
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RESULT 2
AAC74775
ID AAC74775 standard; cDNA; 1505 BP.
XX
AC AAC74775;
XX
DT 08-FEB-2001 (first entry)
XX
DE Human ORFX ORF330 polynucleotide sequence SEQ ID NO:659.
XX
KW Human; open reading frame; ORFX; detection; cytostatic; hepatotropic;
KW vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective;
KW anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant;
KW immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;
KW hypotensive; dermatological; immunosuppressive; antiinflammatory;
KW antiviral; antibacterial; antifungal; antirheumatic; antithyroid;
KW antianaemic; gene therapy; cancer; proliferative disorder; hypertension;
KW neurodegenerative disorder; osteoarthritis; graft vs host disease;
KW cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;
KW cholesterol ester storage; systemic lupus erythematosus; infection;
KW severe combined immunodeficiency; malaria; autoimmune disorder; asthma;
KW allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;
KW bone damage; cartilage damage; antiinflammatory disease; coagulation;
KW thrombosis; contraceptive; ss.
XX
OS Homo sapiens.
XX
PN WO200058473-A2.
XX
PD 05-OCT-2000.
XX
PF 31-MAR-2000; 2000WO-US008621.
XX
PR 31-MAR-1999; 99US-0127607P.
PR 02-APR-1999; 99US-0127636P.
PR 05-APR-1999; 99US-0127728P.
PR 30-MAR-2000; 2000US-00540763.
XX
PA (CURA-) CURAGEN CORP.